

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	716	southern with blot same bacter\$4 same detect\$4	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/05 10:43
L2	591	southern with blot same bacter\$4 same detect\$4 same pcr	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/05 10:43
L3	26	southern with blot same bacter\$4 same detect\$4 same pcr same sample	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/05 10:43



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

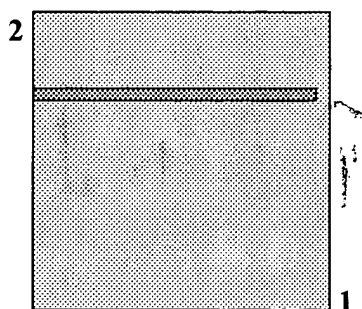
Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2
 x_dropoff: 50 expect: 10.000 wordsize: 11 Filter ☒ Align

Sequence 1 lcl|seq_1 Length 20 (1 .. 20)
 Sequence 2 gi 1799980 E.coli genomic DNA, Kohara clone #436(58.4-58.8 min.). Length 16446 (1 .. 16446)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 39.1 bits (20), Expect = 0.046
 Identities = 20/20 (100%)
 Strand = Plus / Minus

Query: 1 ttcgggttgatcatgccaatg 20
 |||||
 Sbjct: 11799 ttcgggttgatcatgccaatg 11780

SEQ ID NO 2

YAMAMOTO et al.

CPU time: 0.01 user secs. 0.00 sys. secs 0.01 total secs.

Lambda K H
 1.33 0.621 1.12

Gapped
 Lambda K H
 1.33 0.621 1.12

Matrix: blastn matrix:1 -2
 Gap Penalties: Existence: 5, Extension: 2
 Number of Sequences: 1
 Number of Hits to DB: 5

Number of extensions: 1
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 20
Length of database: 13,936,275,478
Length adjustment: 18
Effective length of query: 2
Effective length of database: 13,936,275,460
Effective search space: 27872550920
Effective search space used: 27872550920
Neighboring words threshold: 0
Window for multiple hits: 0
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 16 (31.5 bits)



Blast 2 Sequences results

PubMed

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BLAST

OMIM

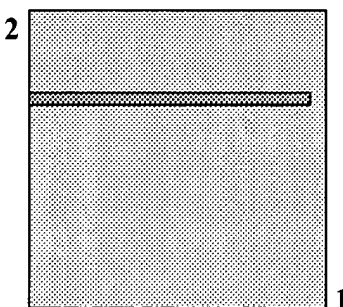
Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2
 x_dropoff: 50 expect: 10.000 wordsize: 11 Filter ☒ Align

Sequence 1 lcl|seq_1 Length 18 (1 .. 18)
 Sequence 2 gi 1799980 E.coli genomic DNA, Kohara clone #436(58.4-58.8 min.). Length 16446 (1 .. 16446)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 35.3 bits (18), Expect = 0.66
 Identities = 18/18 (100%)
 Strand = Plus / Plus

Query: 1 cgcgcaggcaaattctgt 18
 |||||
 Sbjct: 11482 cgcgcaggcaaattctgt 11499

SEQ ID NO 25

YAMAMOTO et al.

CPU time: 0.01 user secs. 0.01 sys. secs 0.02 total secs.

Lambda K H
 1.33 0.621 1.12

Gapped
 Lambda K H
 1.33 0.621 1.12

Matrix: blastn matrix:1 -2
 Gap Penalties: Existence: 5, Extension: 2
 Number of Sequences: 1
 Number of Hits to DB: 4

Number of extensions: 1
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 18
Length of database: 13,936,275,478
Length adjustment: 16
Effective length of query: 2
Effective length of database: 13,936,275,462
Effective search space: 27872550924
Effective search space used: 27872550924
Neighboring words threshold: 0
Window for multiple hits: 0
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 16 (31.5 bits)